Report

	assembly
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4729073
Total length (>= 5000 bp)	4729073
Total length (>= 10000 bp)	4729073
Total length (>= 25000 bp)	4711651
Total length (>= 50000 bp)	4711651
# contigs	2
Largest contig	4711651
Total length	4729073
Reference length	4759746
GC (%)	52.17
Reference GC (%)	52.19
N50	4711651
NG50	4711651
N75	4711651
NG75	4711651
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	4711651
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	8945
Genome fraction (%)	99.175
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.63
# indels per 100 kbp	44.06
Largest alignment	4308301
Total aligned length	4720128
NA50	4308301
NGA50	4308301
NA75	4308301
NGA75	4308301
LA50	1
LGA50	1
LA75	1
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

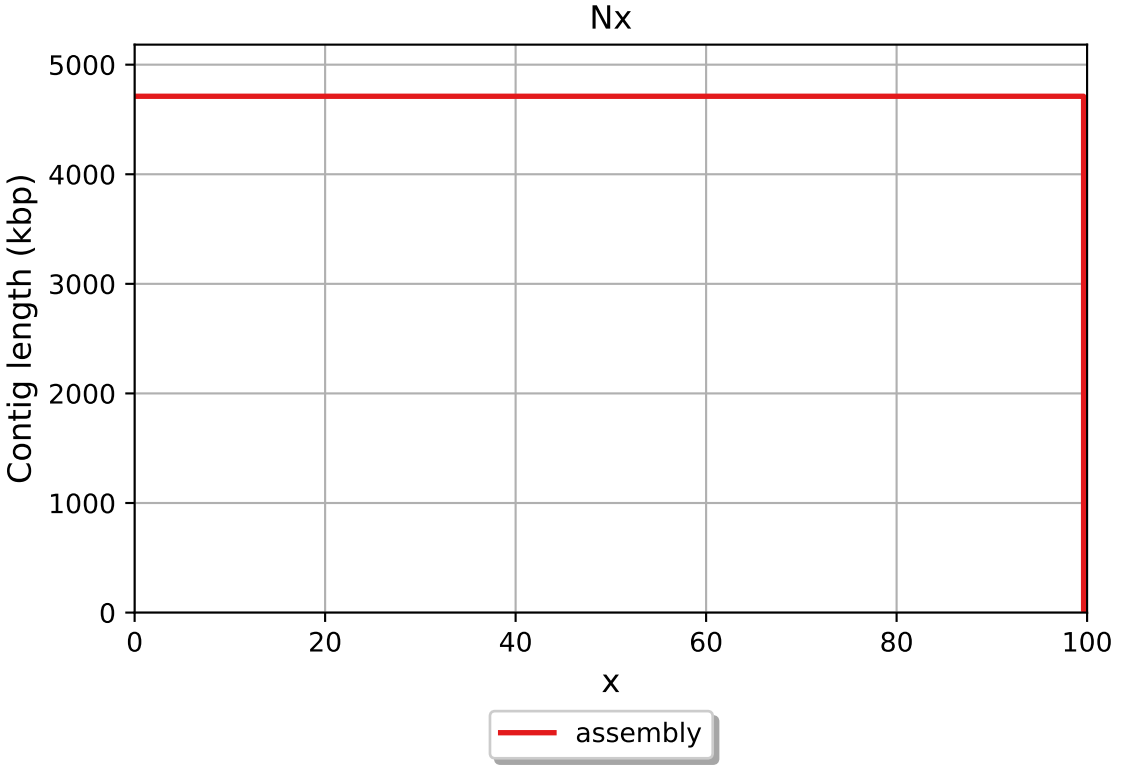
	assembly
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4711651
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1446
# indels	2080
# indels (<= 5 bp)	2075
# indels (> 5 bp)	5
Indels length	2304

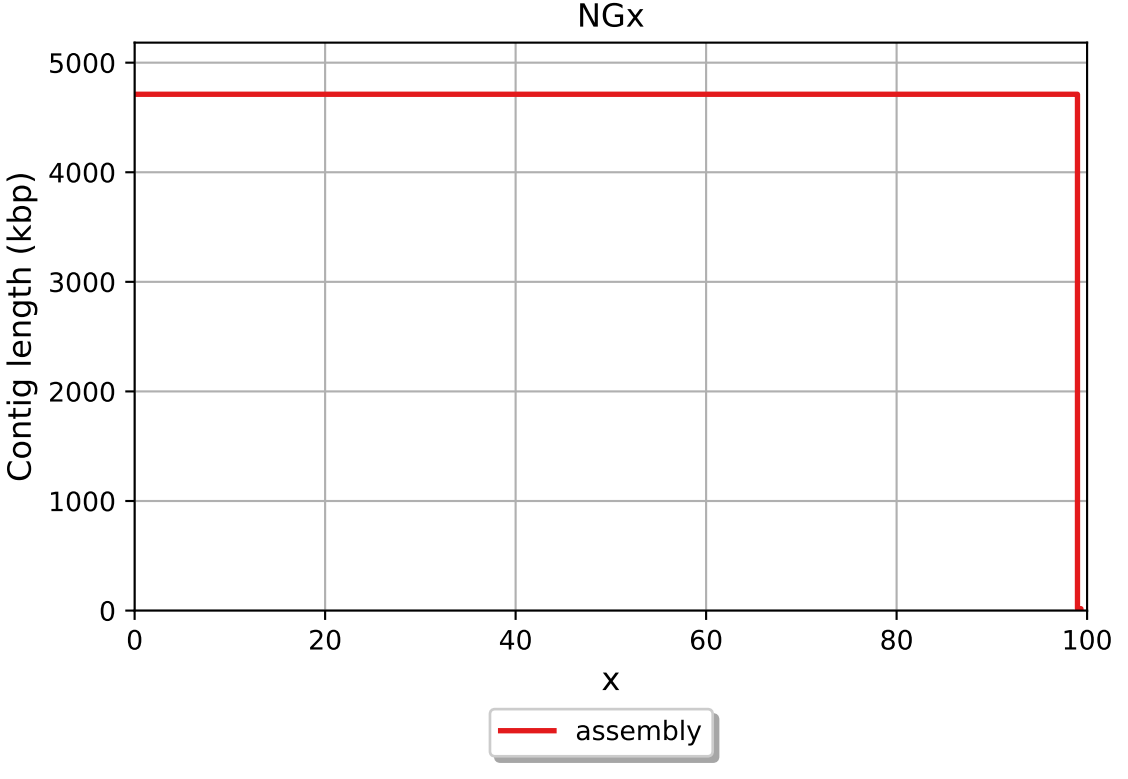
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

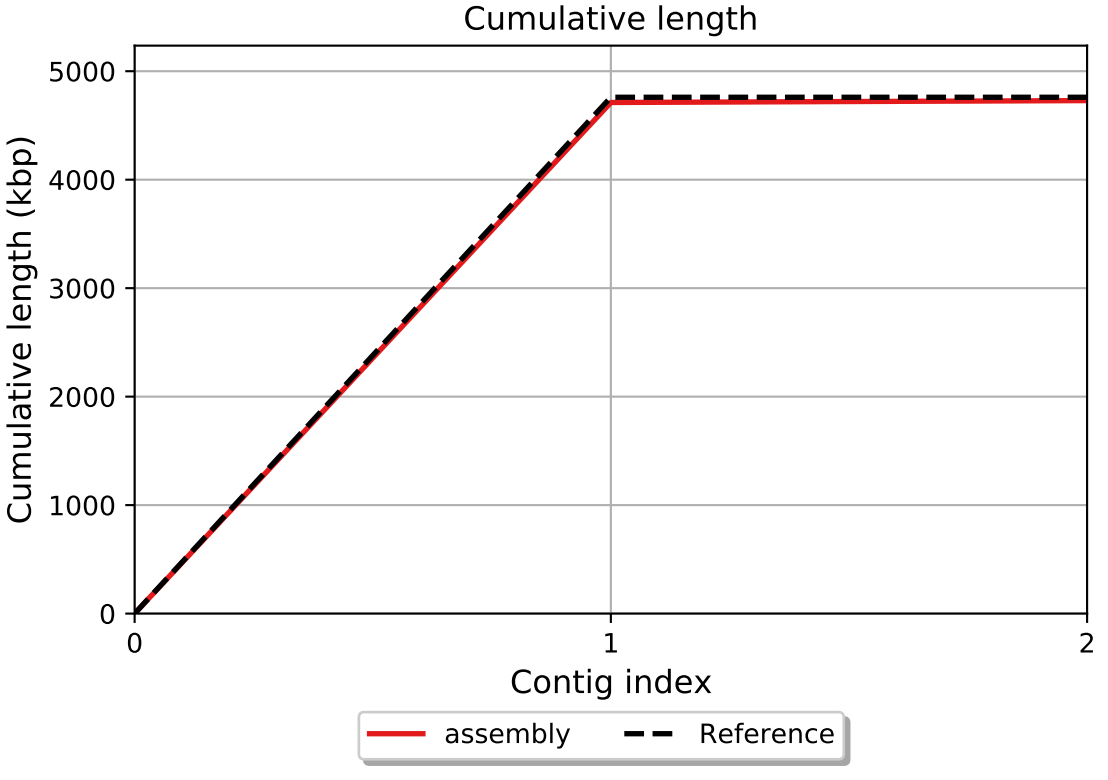
Unaligned report

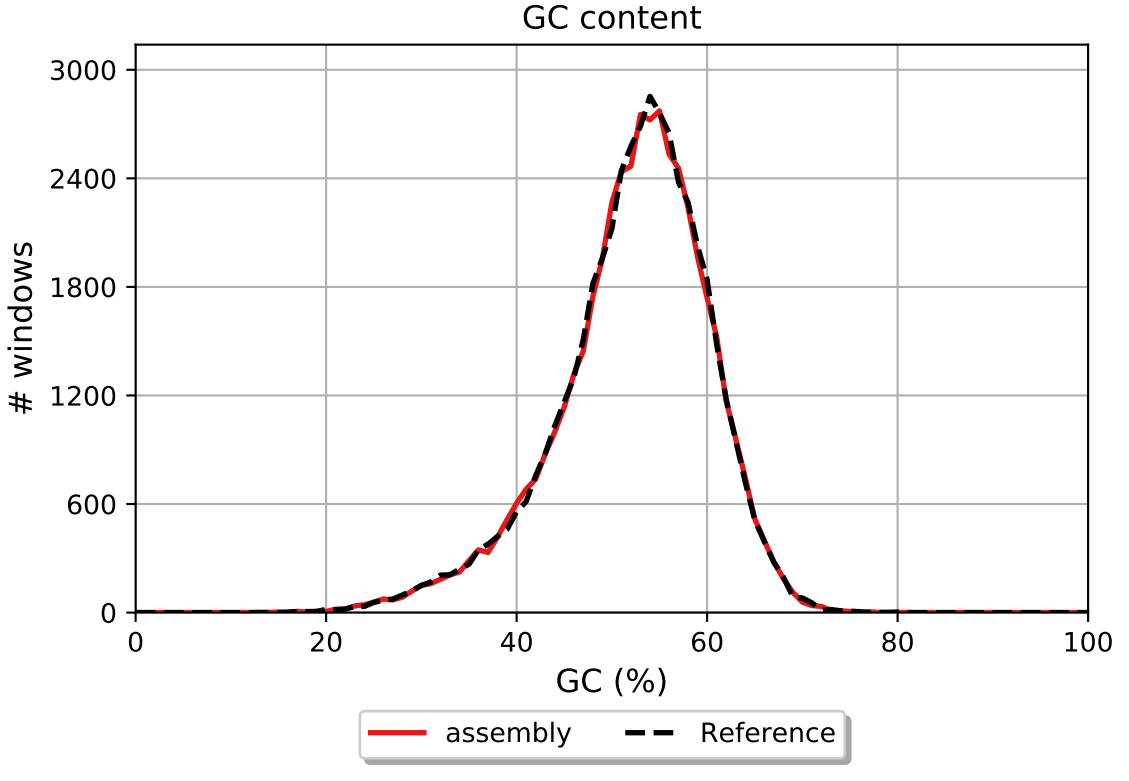
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	8945
# N's	0

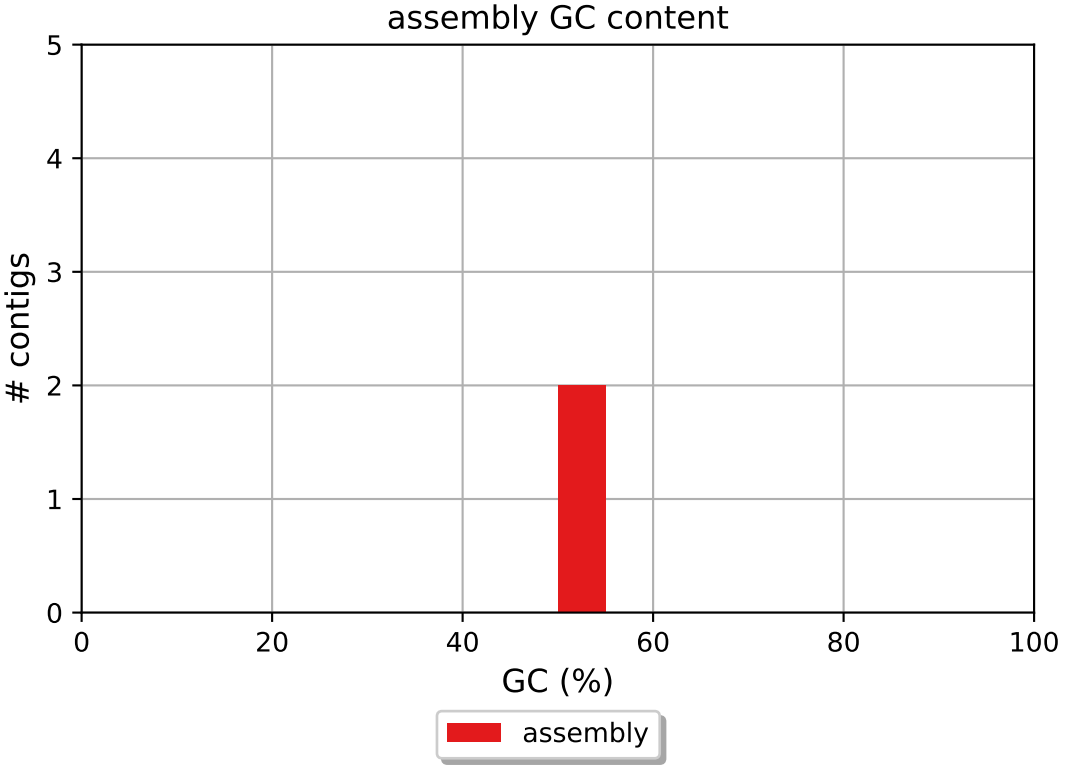
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

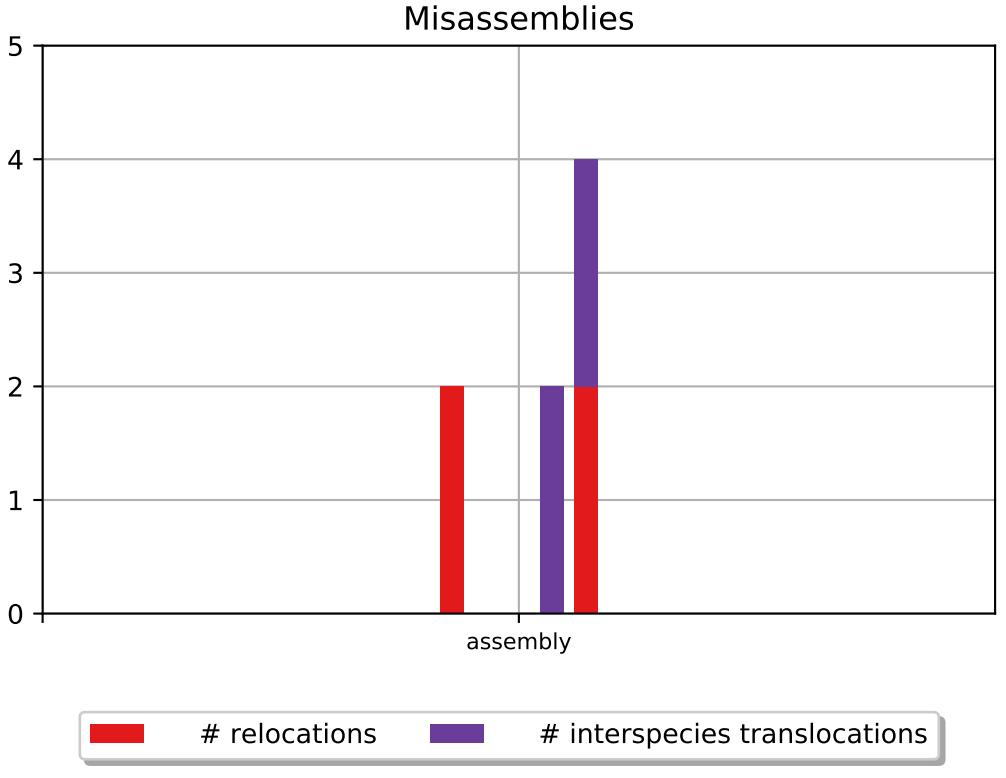

Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
assembly

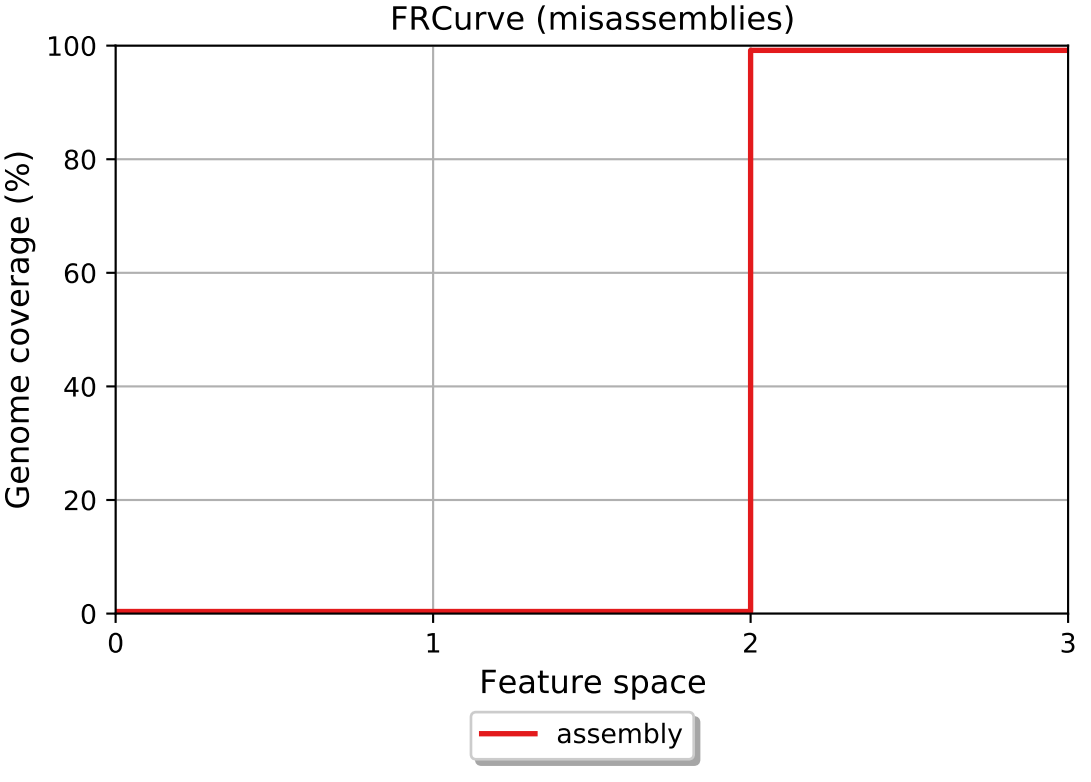

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
assembly

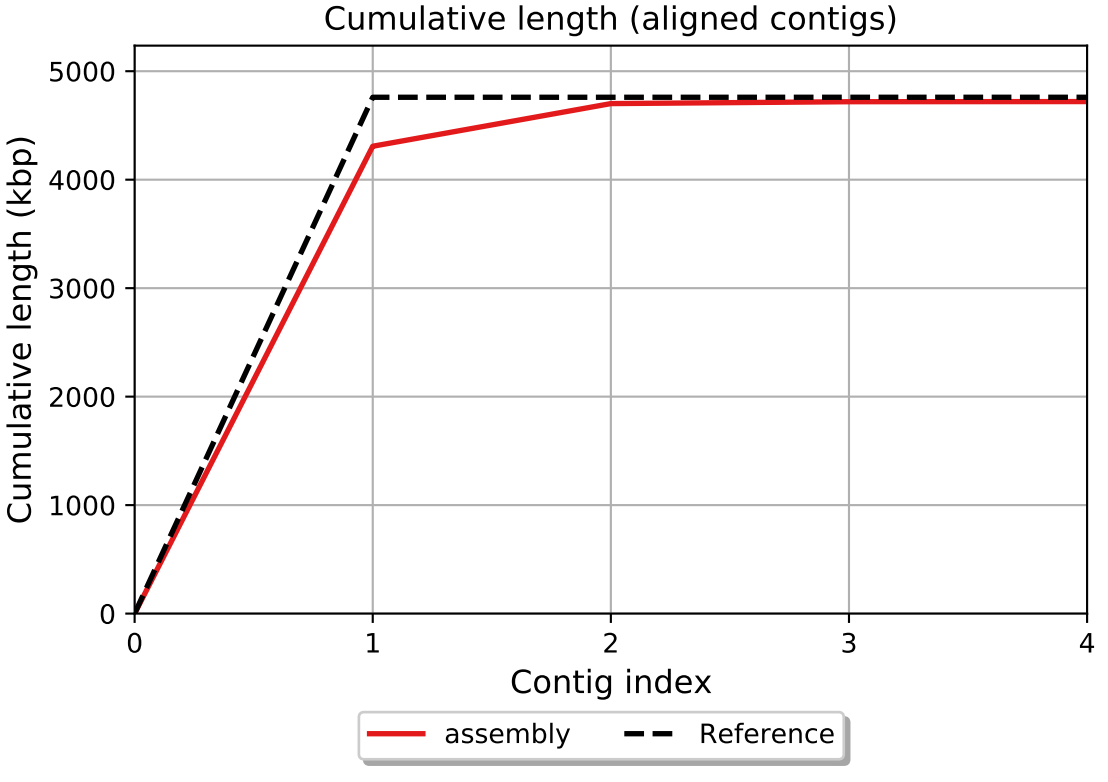

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
Contig index
assembly
Reference

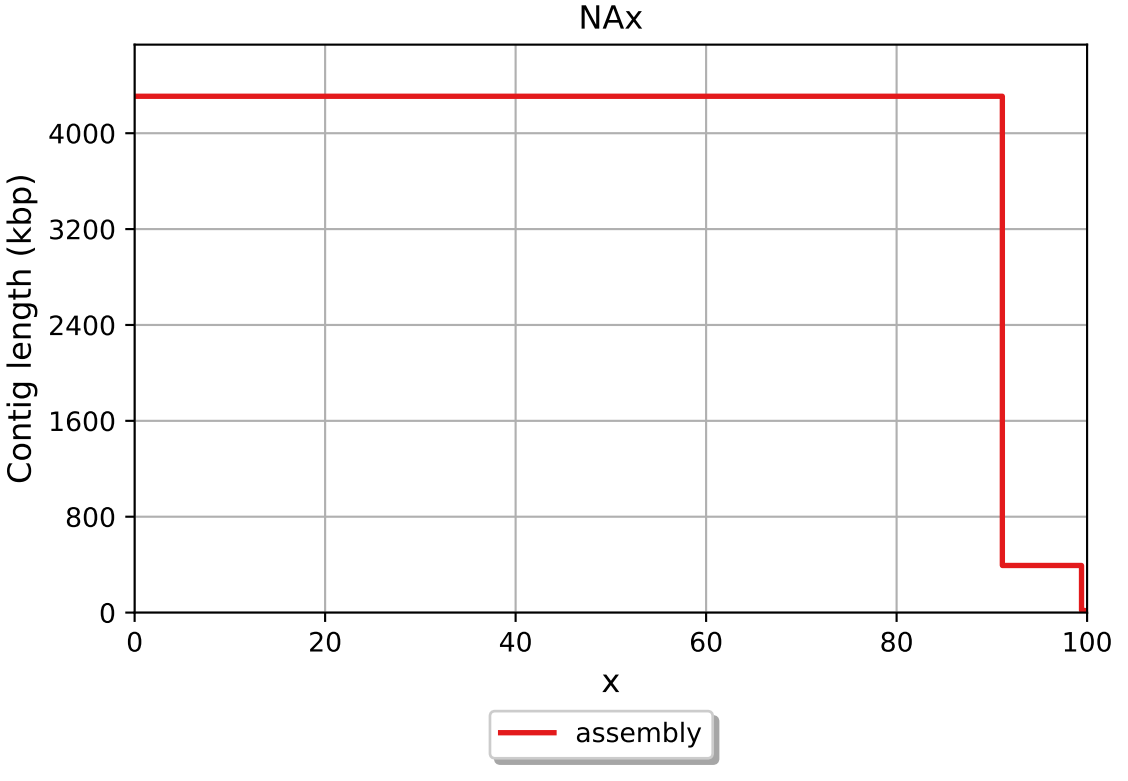

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
assembly
Reference

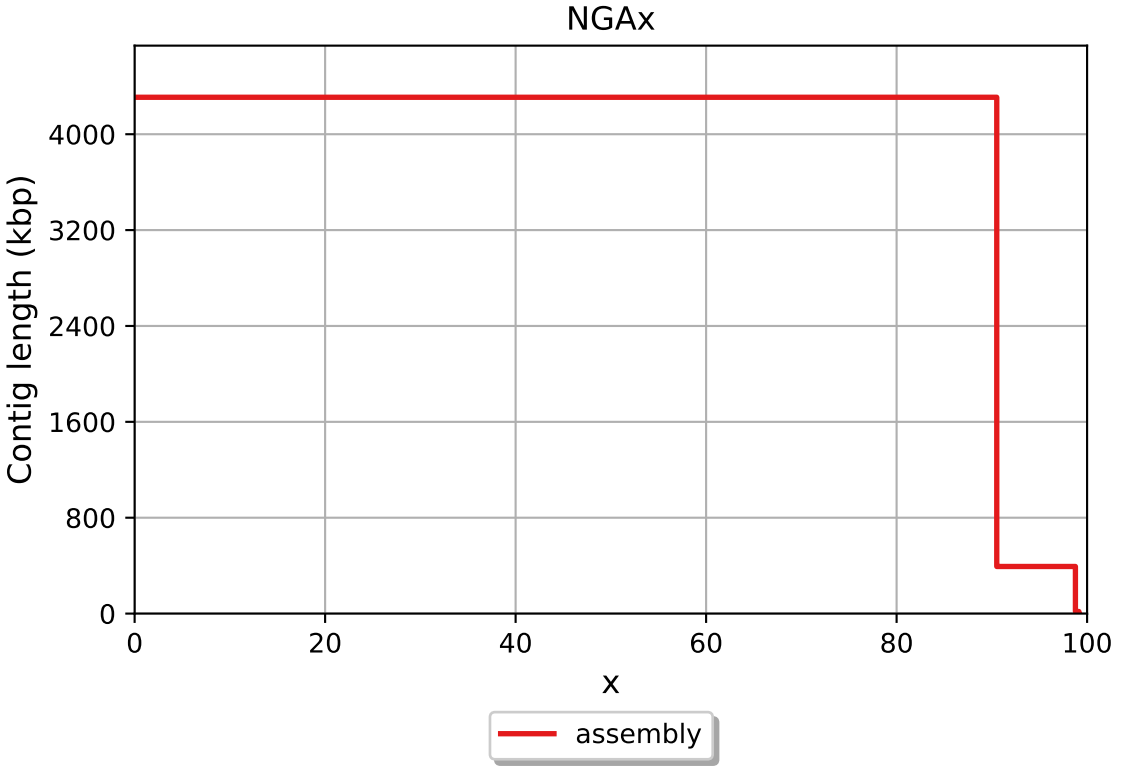

assembly GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assembly


Misassemblies
5
4
3
2
1
0
assembly
relocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
Contig index
assembly
Reference


NAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
assembly


NGAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
assembly